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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2009; month=12; day=22; hr=7; min=36; sec=29; ms=626;]

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Application No: 10575640 Version No: 2.0

Input Set:

Output Set:

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Finished: 2009-12-02 14:52:59.820
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 933 ms
Total Warnings: 6
Total Errors: 0
No. of SeqIDs Defined: 66
Actual SeqID Count: 66

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SEQUENCE LISTING

<110> TURECI, Ozlem
SAHIN, Ugar
KREITER, Sebastian

<120> Recombinant Vaccines and Use Thereof

<130> VOS-120

<140> 10575640

<141> 2009-12-02

<150> PCT/EP2004/011512

<151> 2004-10-13

<150> DE 103 47 710.1

<151> 2003-10-14

<160> 66

<170> PatentIn version 3.1

<210> 1

<211> 78

<212> DNA

<213> Homo sapiens

<400> 1

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<210> 2

<211> 26

<212> PRT

<213> Homo sapiens

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Met Arg Val Thr Ala Pro Arg Thr Leu Ile Leu Leu Leu Ser Gly Ala

1 5 10 15

Leu Ala Leu Thr Glu Thr Trp Ala Gly Ser

20 25

<210> 3

<211> 168

<212> DNA

<213> Homo sapiens

<400> 3

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gcgtccagcg acagtgccca gggctctgat gtgtctctca cagcttga 168

<210> 4
<211> 55
<212> PRT
<213> Homo sapiens

<400> 4

Ile Val Gly Ile Val Ala Gly Leu Ala Val Leu Ala Val Val Val Ile
1 5 10 15

Gly Ala Val Val Ala Thr Val Met Cys Arg Arg Lys Ser Ser Gly Gly
20 25 30

Lys Gly Gly Ser Tyr Ser Gln Ala Ala Ser Ser Asp Ser Ala Gln Gly
35 40 45

Ser Asp Val Ser Leu Thr Ala
50 55

<210> 5
<211> 129
<212> DNA
<213> Homo sapiens

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ctgagctga 129

<210> 6
<211> 42
<212> PRT
<213> Homo sapiens

<400> 6

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1 5 10 15

Phe Leu Gly Ala Gly Leu Phe Ile Tyr Phe Arg Asn Gln Lys Gly His
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Ser Gly Leu Gln Pro Arg Gly Phe Leu Ser
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<210> 7
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA of restriction site in human HLA class I domains

<400> 7
ctgcaggtcg actctagagg atcc 24

<210> 8
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Restriction site in human HLA class I domains

<400> 8

Leu Gln Val Asp Ser Arg Gly Ser
1 5

<210> 9
<211> 1683
<212> DNA
<213> Human cytomegalovirus

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<210> 10

<211> 561

<212> PRT

<213> Human cytomegalovirus

<400> 10

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Pro Ile Ser Gly His Val Leu Lys Ala Val Phe Ser Arg Gly Asp Thr
20 25 30

Pro Val Leu Pro His Glu Thr Arg Leu Leu Gln Thr Gly Ile His Val
35 40 45

Arg Val Ser Gln Pro Ser Leu Ile Leu Val Ser Gln Tyr Thr Pro Asp
50 55 60

Ser Thr Pro Cys His Arg Gly Asp Asn Gln Leu Gln Val Gln His Thr
65 70 75 80

Tyr Phe Thr Gly Ser Glu Val Glu Asn Val Ser Val Asn Val His Asn
85 90 95

Pro Thr Gly Arg Ser Ile Cys Pro Ser Gln Glu Pro Met Ser Ile Tyr
100 105 110

Val Tyr Ala Leu Pro Leu Lys Met Leu Asn Ile Pro Ser Ile Asn Val
115 120 125

His His Tyr Pro Ser Ala Ala Glu Arg Lys His Arg His Leu Pro Val
130 135 140

Ala Asp Ala Val Ile His Ala Ser Gly Lys Gln Met Trp Gln Ala Arg
145 150 155 160

Leu Thr Val Ser Gly Leu Ala Trp Thr Arg Gln Gln Asn Gln Trp Lys
165 170 175

Glu Pro Asp Val Tyr Tyr Thr Ser Ala Phe Val Phe Pro Thr Lys Asp
180 185 190

Val Ala Leu Arg His Val Val Cys Ala His Glu Leu Val Cys Ser Met
195 200 205

Glu Asn Thr Arg Ala Thr Lys Met Gln Val Ile Gly Asp Gln Tyr Val
210 215 220

Lys Val Tyr Leu Glu Ser Phe Cys Glu Asp Val Pro Ser Gly Lys Leu
225 230 235 240

Phe Met His Val Thr Leu Gly Ser Asp Val Glu Glu Asp Leu Thr Met
245 250 255

Thr Arg Asn Pro Gln Pro Phe Met Arg Pro His Glu Arg Asn Gly Phe
260 265 270

Thr Val Leu Cys Pro Lys Asn Met Ile Ile Lys Pro Gly Lys Ile Ser

275

280

285

His Ile Met Leu Asp Val Ala Phe Thr Ser His Glu His Phe Gly Leu
290 295 300

Leu Cys Pro Lys Ser Ile Pro Gly Leu Ser Ile Ser Gly Asn Leu Leu
305 310 315 320

Met Asn Gly Gln Gln Ile Phe Leu Glu Val Gln Ala Ile Arg Glu Thr
325 330 335

Val Glu Leu Arg Gln Tyr Asp Pro Val Ala Ala Leu Phe Phe Phe Asp
340 345 350

Ile Asp Leu Leu Leu Gln Arg Gly Pro Gln Tyr Ser Glu His Pro Thr
355 360 365

Phe Thr Ser Gln Tyr Arg Ile Gln Gly Lys Leu Glu Tyr Arg His Thr
370 375 380

Trp Asp Arg His Asp Glu Gly Ala Ala Gln Gly Asp Asp Asp Val Trp
385 390 395 400

Thr Ser Gly Ser Asp Ser Asp Glu Glu Leu Val Thr Thr Glu Arg Lys
405 410 415

Thr Pro Arg Val Thr Gly Gly Gly Ala Met Ala Gly Ala Ser Thr Ser
420 425 430

Ala Gly Arg Lys Arg Lys Ser Ala Ser Ser Ala Thr Ala Cys Thr Ser
435 440 445

Gly Val Met Thr Arg Gly Arg Leu Lys Ala Glu Ser Thr Val Ala Pro
450 455 460

Glu Glu Asp Thr Asp Glu Asp Ser Asp Asn Glu Ile His Asn Pro Ala
465 470 475 480

Val Phe Thr Trp Pro Pro Trp Gln Ala Gly Ile Leu Ala Arg Asn Leu
485 490 495

Val Pro Met Val Ala Thr Val Gln Gly Gln Asn Leu Lys Tyr Gln Glu
500 505 510

Phe Phe Trp Asp Ala Asn Asp Ile Tyr Arg Ile Phe Ala Glu Leu Glu
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Gly Val Trp Gln Pro Ala Ala Gln Pro Lys Arg Arg Arg His Arg Gln
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Asp Ala Leu Pro Gly Pro Cys Ile Ala Ser Thr Pro Lys Lys His Arg
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Gly

<210> 11
<211> 1962
<212> DNA
<213> Artificial Sequence

<220>
<223> DNA encoding human HLA class I domains and CMV pp65

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cgccgttggtc ccgaaatgat atccgtactg ggtcccatTT cggggcacgt gctgaaagcc 180
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tgctccatgg agaacacgcg cgcaaccaag atgcagggtga taggtgacca gtacgtcaag 780
gtgtacctgg agtccttctg cgaggacgtg ccctccggca agctctttat gcacgtcacg 840
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<210> 12

<211> 653

<212> PRT

<213> Artificial Sequence

<220>

<223> Fusion protein of human HLA class I domains and CMV pp65

<400> 12

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Met Arg Val Thr Ala Pro Arg Thr Leu Ile Leu Leu Leu Ser Gly Ala
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Leu Ala Leu Thr Glu Thr Trp Ala Gly Ser Leu Gln Val Asp Ser Arg
20           25           30

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Gly Ser Thr Met Glu Ser Arg Gly Arg Arg Cys Pro Glu Met Ile Ser
35           40           45

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Val Leu Gly Pro Ile Ser Gly His Val Leu Lys Ala Val Phe Ser Arg
50 55 60

Gly Asp Thr Pro Val Leu Pro His Glu Thr Arg Leu Leu Gln Thr Gly
65 70 75 80

Ile His Val Arg Val Ser Gln Pro Ser Leu Ile Leu Val Ser Gln Tyr
85 90 95

Thr Pro Asp Ser Thr Pro Cys His Arg Gly Asp Asn Gln Leu Gln Val
100 105 110

Gln His Thr Tyr Phe Thr Gly Ser Glu Val Glu Asn Val Ser Val Asn
115 120 125

Val His Asn Pro Thr Gly Arg Ser Ile Cys Pro Ser Gln Glu Pro Met
130 135 140

Ser Ile Tyr Val Tyr Ala Leu Pro Leu Lys Met Leu Asn Ile Pro Ser
145 150 155 160

Ile Asn Val His His Tyr Pro Ser Ala Ala Glu Arg Lys His Arg His
165 170 175

Leu Pro Val Ala Asp Ala Val Ile His Ala Ser Gly Lys Gln Met Trp
180 185 190

Gln Ala Arg Leu Thr Val Ser Gly Leu Ala Trp Thr Arg Gln Gln Asn
195 200 205

Gln Trp Lys Glu Pro Asp Val Tyr Tyr Thr Ser Ala Phe Val Phe Pro
210 215 220

Thr Lys Asp Val Ala Leu Arg His Val Val Cys Ala His Glu Leu Val
225 230 235 240

Cys Ser Met Glu Asn Thr Arg Ala Thr Lys Met Gln Val Ile Gly Asp
245 250 255

Gln Tyr Val Lys Val Tyr Leu Glu Ser Phe Cys Glu Asp Val Pro Ser
260 265 270

Gly	Lys	Leu	Phe	Met	His	Val	Thr	Leu	Gly	Ser	Asp	Val	Glu	Glu	Asp	275	280	285
Leu	Thr	Met	Thr	Arg	Asn	Pro	Gln	Pro	Phe	Met	Arg	Pro	His	Glu	Arg	290	295	300
Asn	Gly	Phe	Thr	Val	Leu	Cys	Pro	Lys	Asn	Met	Ile	Ile	Lys	Pro	Gly	305	310	315
Lys	Ile	Ser	His	Ile	Met	Leu	Asp	Val	Ala	Phe	Thr	Ser	His	Glu	His	325	330	335
Phe	Gly	Leu	Leu	Cys	Pro	Lys	Ser	Ile	Pro	Gly	Leu	Ser	Ile	Ser	Gly	340	345	350
Asn	Leu	Leu	Met	Asn	Gly	Gln	Gln	Ile	Phe	Leu	Glu	Val	Gln	Ala	Ile	355	360	365
Arg	Glu	Thr	Val	Glu	Leu	Arg	Gln	Tyr	Asp	Pro	Val	Ala	Ala	Leu	Phe	370	375	380
Phe	Phe	Asp	Ile	Asp	Leu	Leu	Leu	Gln	Arg	Gly	Pro	Gln	Tyr	Ser	Glu	385	390	395
His	Pro	Thr	Phe	Thr	Ser	Gln	Tyr	Arg	Ile	Gln	Gly	Lys	Leu	Glu	Tyr	405	410	415
Arg	His	Thr	Trp	Asp	Arg	His	Asp	Glu	Gly	Ala	Ala	Gln	Gly	Asp	Asp	420	425	430
Asp	Val	Trp	Thr	Ser	Gly	Ser	Asp	Ser	Asp	Glu	Glu	Leu	Val	Thr	Thr	435	440	445
Glu	Arg	Lys	Thr	Pro	Arg	Val	Thr	Gly	Gly	Gly	Ala	Met	Ala	Gly	Ala	450	455	460
Ser	Thr	Ser	Ala	Gly	Arg	Lys	Arg	Lys	Ser	Ala	Ser	Ser	Ala	Thr	Ala	465	470	475
Cys	Thr	Ser	Gly	Val	Met	Thr	Arg	Gly	Arg	Leu	Lys	Ala	Glu	Ser	Thr	485	490	495

Val Ala Pro Glu Glu Asp Thr Asp Glu Asp Ser Asp Asn Glu Ile His
500 505 510

Asn Pro Ala Val Phe Thr Trp Pro Pro Trp Gln Ala Gly Ile Leu Ala
515 520 525

Arg Asn Leu Val Pro Met Val Ala Thr Val Gln Gly Gln Asn Leu Lys
530 535 540

Tyr Gln Glu Phe Phe Trp Asp Ala Asn Asp Ile Tyr Arg Ile Phe Ala
545 550 555 560

Glu Leu Glu Gly Val Trp Gln Pro Ala Ala Gln Pro Lys Arg Arg Arg
565 570 575

His Arg Gln Asp Ala Leu Pro Gly Pro Cys Ile Ala Ser Thr Pro L